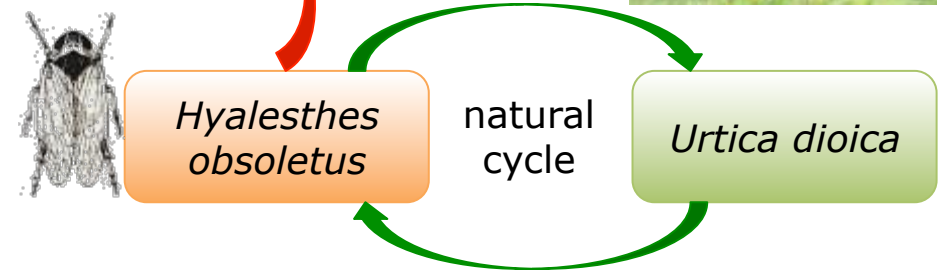
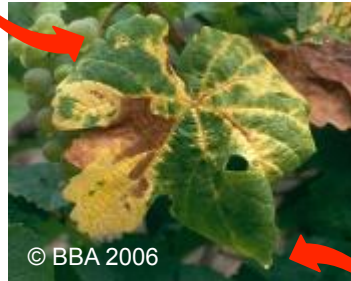
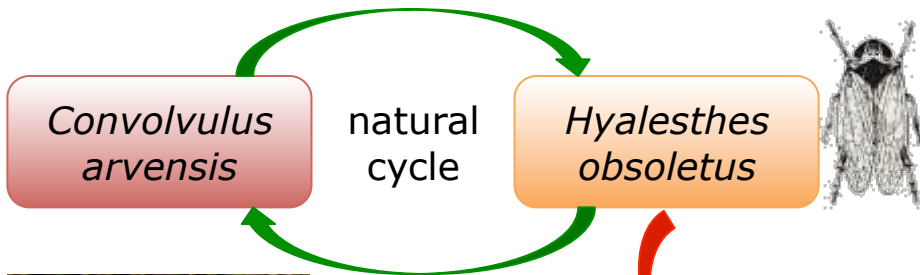


Microsatellite Markers
for the Study of
Host Races and Dispersal Biology
of the Bois Noir Grapevine Yellows Vector
Hyalesthes obsoletus

Miriam Imo, Michael Maixner,
Jes Johannesen



Does *Hyalesthes*
obsoletus have **host**
races adapted to
bindweed and nettle?

- phenological differences between the two vector populations
- plant-specific stolbur strains

→ genetic differences???

Does *Hyalesthes obsoletus* have genetic host races?

Genetic differentiation between nettle and bindweed populations

Probably...

problem with mtDNA, RAPD-DNA, allozymes:
very little genetic variation

Microsatellites

testing 18 isolates

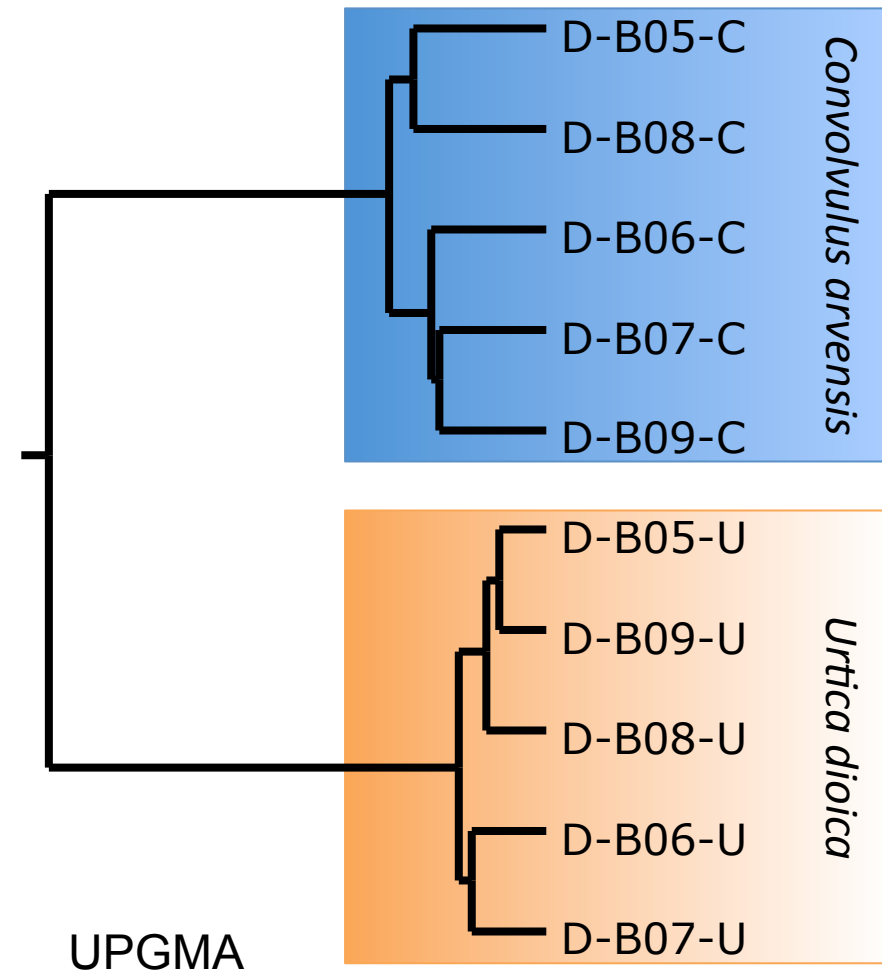
Microsatellite analysis

- 7 microsatellite loci show reliable and consistent results
 - 13 to 28 alleles (mean 19)
 - gene diversity of 0.69 to 0.80 (mean 0.75)
 - 6 loci in Hardy-Weinberg equilibrium
 - 1 locus sex-linked
 - 1 locus not in HWE
- multiplex analysis allows for time- and cost efficient analysis

Does *Hyalesthes obsoletus* have genetic host races?

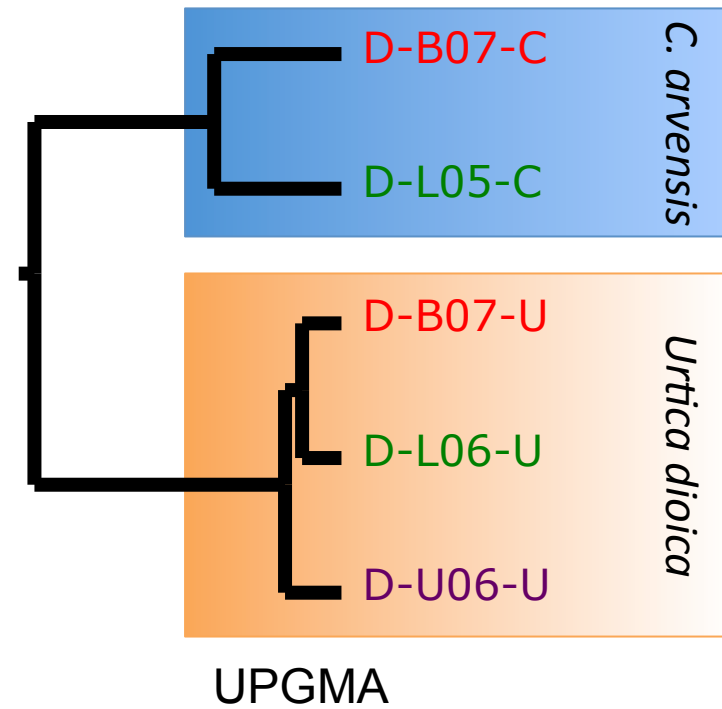
Genetic differentiation between nettle and bindweed populations

- analysis of German *Hyalesthes obsoletus* populations
 - from one site (Bacharach, Rhine)
 - both host plants
 - over 5 years
- clear distinction between two host plants



Does *Hyalesthes obsoletus* have genetic host races?

Genetic differentiation between nettle and bindweed populations



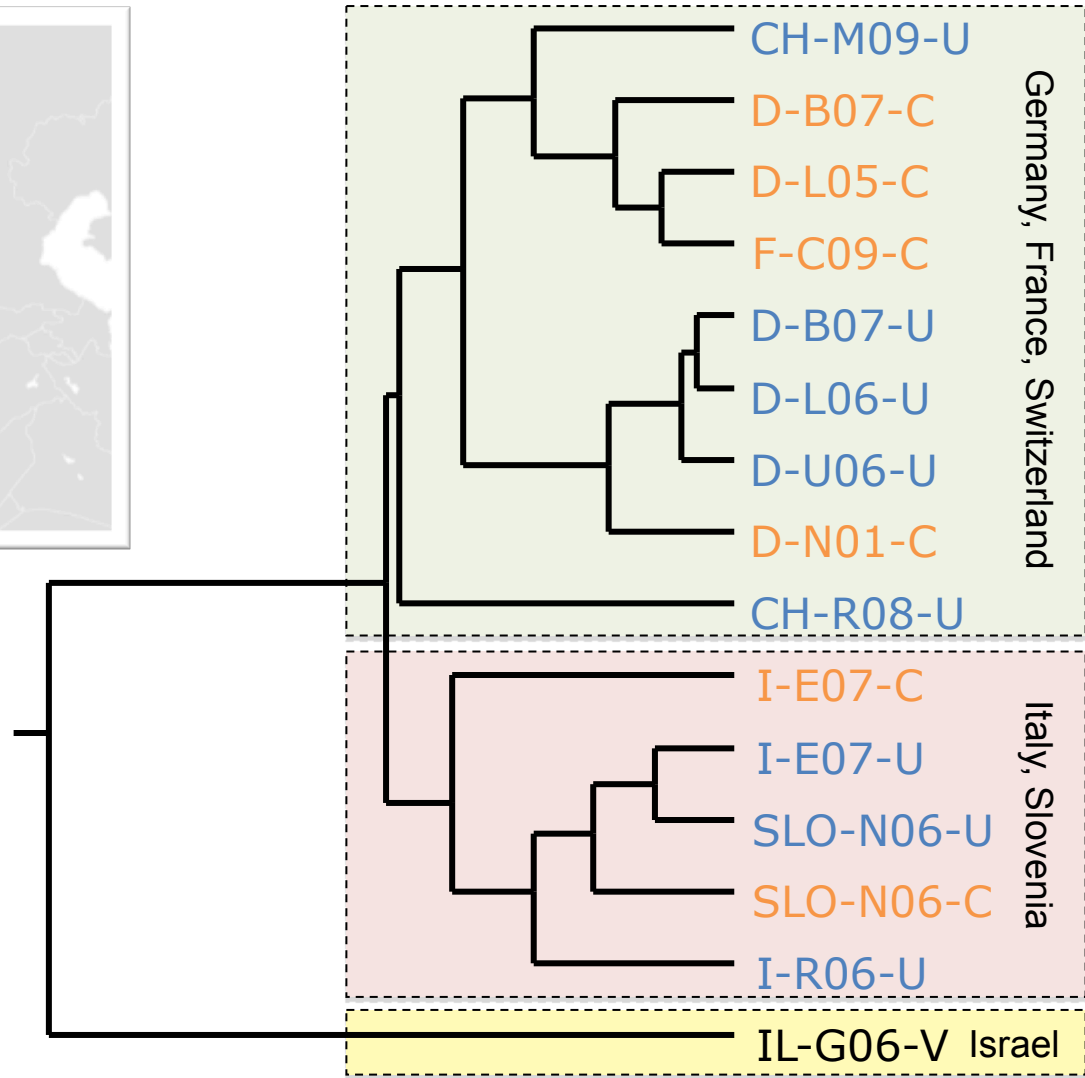
Does *Hyalesthes obsoletus* have genetic host races?

Genetic differentiation between nettle and bindweed populations

- shallow diversification in RAPD and mtDNA rules out old host races of *Hyalesthes obsoletus*
- diversification in microsatellites & phenotypic differences indicate on-going host-plant specialization
- if analysed separately, all loci produce (almost) the same results → indicates that genetic drift, rather than selection, causes split between nettle and bindweed populations

Does *Hyalesthes obsoletus* have genetic host races?

Genetic differentiation between nettle and bindweed populations



→ no distinction between host races

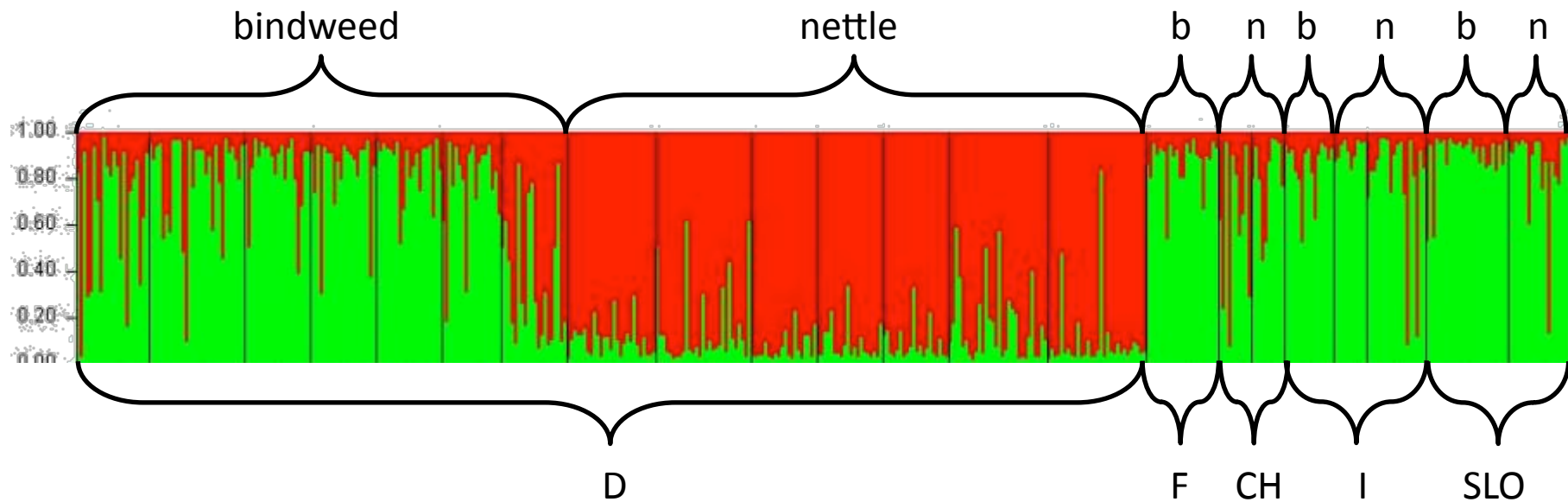
→ more samples needed

UPGMA

Does *Hyalesthes obsoletus* have genetic host races?

Genetic differentiation between nettle and bindweed populations

Structure analysis, K=2



Next steps

- continuing microsatellite analysis of all available populations
- sampling further populations from Slovenia, Switzerland, Germany, ... next summer
- monitoring infestation of vineyards (cooperation with JKI)
- „co-mapping“ of host-specificity and geographic distribution of vector and stolbur pathogen